App. No. 10/723,908
October 31, 2007

AMENDMENTS TO THE SPECIFICATION

PLEASE AMEND THE SPECIFICATION AS FOLLOWS:

Please replace the first paragraph on page 1 of the Specification with the following:

This application is a continuation of ~~co-pending~~abandoned U.S. Patent Application No. 09/615,947, filed on July 13 2000, the entire contents of which are hereby incorporated by reference. This application also reclaims priority under 35 U.S.C. § 120/119 to Danish Application No. PA 1999 01020, filed on July 13, 1999, and U.S. Provisional Patent No. 60/144,011, filed on July 15, 1999.

Please replace lines 1-8 of page 6 of the Specification with the following:

N_{ref}=8). A gap is counted as non-identity of the specific residue(s), i.e. the DNA sequence AGTGTC will have a sequence identity of 75% with the DNA sequence AGTCAGTC (N_{dif}=2 and N_{ref}=8). Sequence identity can alternatively be calculated by the BLAST program e.g. the BLASTP program (Pearson W.R and D.J. Lipman (1988) PNAS USA 85:2444-2448)~~(www.ncbi.nlm.nih.gov/cgi-bin/BLAST)~~. In one aspect of the invention, alignment is performed with the global align algorithm with default parameters as described by X. Huang and W. Miller. Adv. Appl. Math. (1991) 12:337-357.~~, available at http://www.ch.embnet.org/software/LALIGN_form.html.~~

KG   **Please replace line ~~30~~ 35 of page ~~35~~ 30 of the Specification with the following line:**

The fact that certain of the disclosed antigens are not ~~pre??ent~~present in *M. bovis* BCG but are

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